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A

```

OsMAPK5a -----MDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVFN
OsMAPK5b -----MDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVFN
TaWCK-1 -----MDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVFN
NWIPK  MADANMGAGGQGFDPFVSVLTHGGQYVQFDIFGNFEETIT
Consensus MDGAPVAEFRPTMTHGGR LLY IFGN FE T

I II
OsMAPK5a KYOPPIMPPIGRGAYGIVCSVMNFETREMVAIKKIANAFNN
OsMAPK5b KYOPPIMPPIGRGAYGIVCSVMNFETREMVAIKKIAN----
TaWCK-1 KYOPPIMPPIGRGAYGIVCSVMNFETREMVAISKKIANAFNN
NWIPK  KYRPPIMPPIGRGAYGIVCSVLNTELNMVAVKKIANAFDI
Consensus KYOPPIMPPIGRGAYGIVCSVMNFETREMVAIKKIANAF N

III IV
OsMAPK5a DMDAKRTLREIKLLRHLHDHENIIGIRDVI PPPIPOAFNDV
OsMAPK5b NMDAKRTLREIKLLRHLHDHENIVGLRDVI PPPIPOAFNDV
TaWCK-1 YMDAKRTLREIKLLRHLHDHENIVGLRDVI PPPIPOAFNDV
NWIPK  YMDAKRTLREIKLLRHLHDHENIVGLRDVI PPPIPOAFNDV
Consensus MDAKRTLREIKLLRHLHDHENIIGIRDVI PP IP FNDV

V
OsMAPK5a YIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYI
OsMAPK5b YIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYI
TaWCK-1 YIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYI
NWIPK  YIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYI
Consensus YIATELMDTDLHHIIRSNQELSEEHCQYFLYQILRGLKYI

VI VII
OsMAPK5a HSA NVIHRDLKPSNLLLNANCDLKICDFGLARPSSSESDMM
OsMAPK5b -----CDLKICDFGLARPSSSESDMM
TaWCK-1 HSA NVIHRDLKPSNLLLNANCDLKICDFGLARPSSSESDMM
NWIPK  HSA NVIHRDLKPSNLLLNANCDLKICDFGLARPSSSESDMM
Consensus HSA NVIHRDLKPSNLLLNANCDLKICDFGLARPSSSESDMM

* * VIII IX
OsMAPK5a TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIFMELINR
OsMAPK5b TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIFMELINR
TaWCK-1 TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIFMELINR
NWIPK  TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIFMELINR
Consensus TEYVVTRWYRAPELLNSTDYSAIDVWSVGCIFMELINR

X
OsMAPK5a OPLFPGRDHMHQRLITEVIGTPTDDELGFIRNEDARKYM
OsMAPK5b OPLFPGRDHMHQRLITEVIGTPTDDELGFIRNEDARKYM
TaWCK-1 OPLFPGRDHMHQRLITEVIGTPTDDELGFIRNEDARKYM
NWIPK  KPLFGGKDHVHQRLLITELLGTPTDDELGFIRNEDARKYM
Consensus PLFPGRDHMHQRLITEVIGTPTDD LGFIRNEDARKYM

XI
OsMAPK5a RHLPOYPRRTFASMFPRVQPAALDLIERMLTFNPLQRTTV
OsMAPK5b RHLPOYPRRTFASMFPRVQPAALDLIERMLTFNPLQRTTV
TaWCK-1 RHLPOYPRRTFASMFPRVQPAALDLIERMLTFNPLQRTTV
NWIPK  RHLPOYPRRTFASMFPRVQPAALDLIERMLTFNPLQRTTV
Consensus RHLPOYPRRTFASMFPRVQPAALDLIERMLTFNPLQRTTV

OsMAPK5a EEALDHPYLERLHDIADEPTICLPFSDFEOKALNEDOMK
OsMAPK5b EEALDHPYLERLHDIADEPTICLPFSDFEOKALNEDOMK
TaWCK-1 EEALDHPYLERLHDIADEPTICLPFSDFEOKALNEDOMK
NWIPK  EEALDHPYLERLHDIADEPTICLPFSDFEOKALNEDOMK
Consensus EEALDHPYLERLHDIADEPTICLPFSDFEOKALNEDOMK

OsMAPK5a OLIFNEAIEEMNPNI RY
OsMAPK5b OLIFNEAIEEMNPNI RY
TaWCK-1 OLIFNEAIEEMNPNI RY
NWIPK  OLIFNEAIEEMNPNI RY
Consensus OLIFNEAIEEMNPNI RY

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B

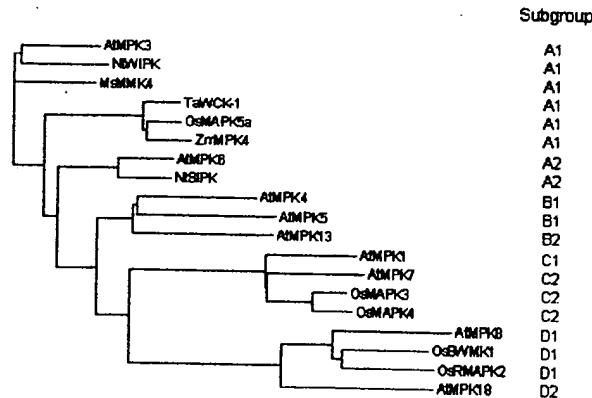


FIGURE 1

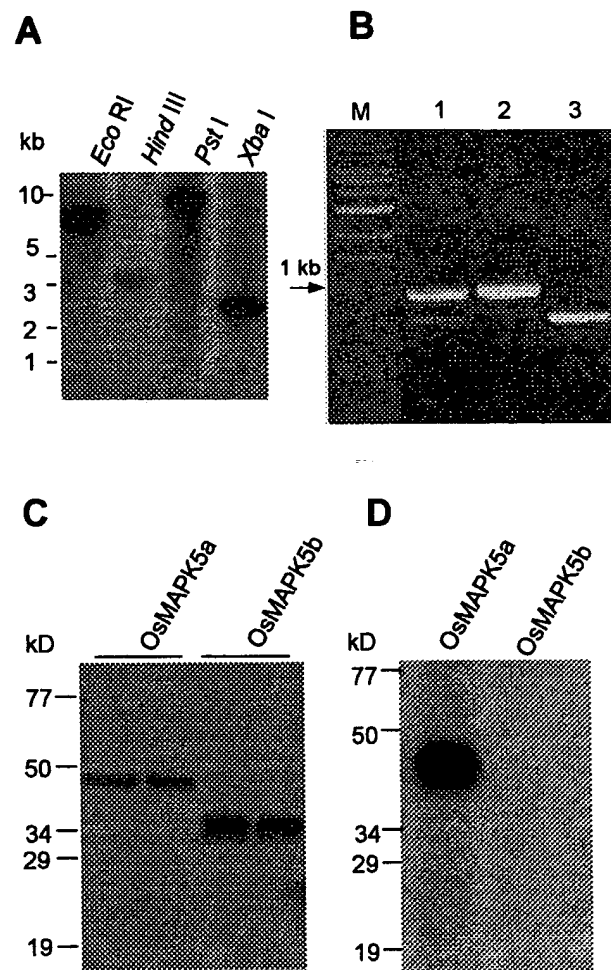


FIGURE 2

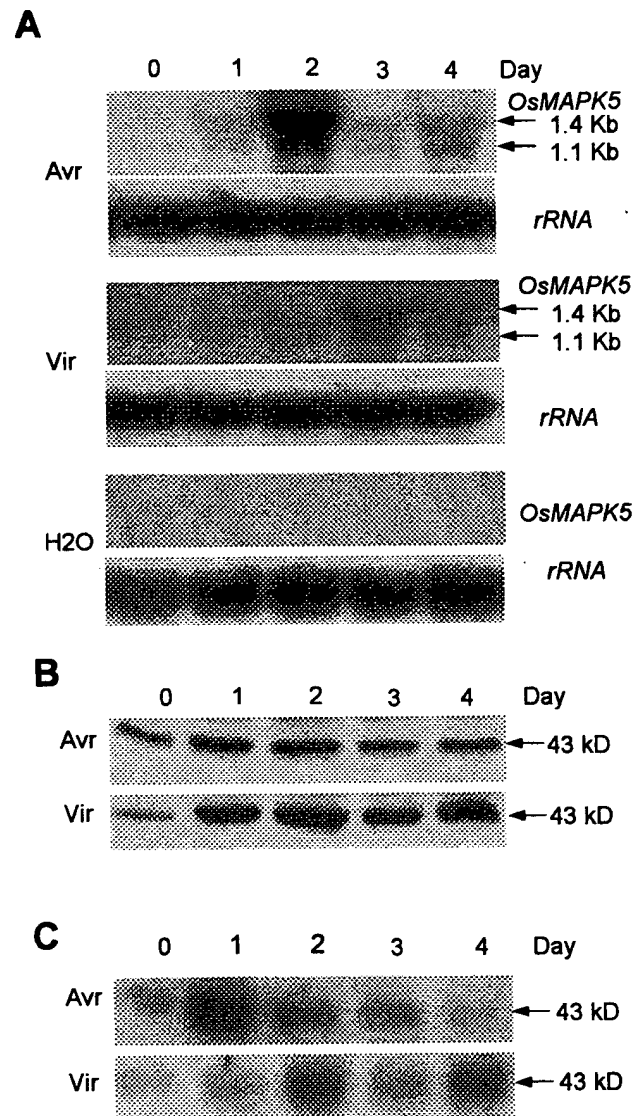


FIGURE 3

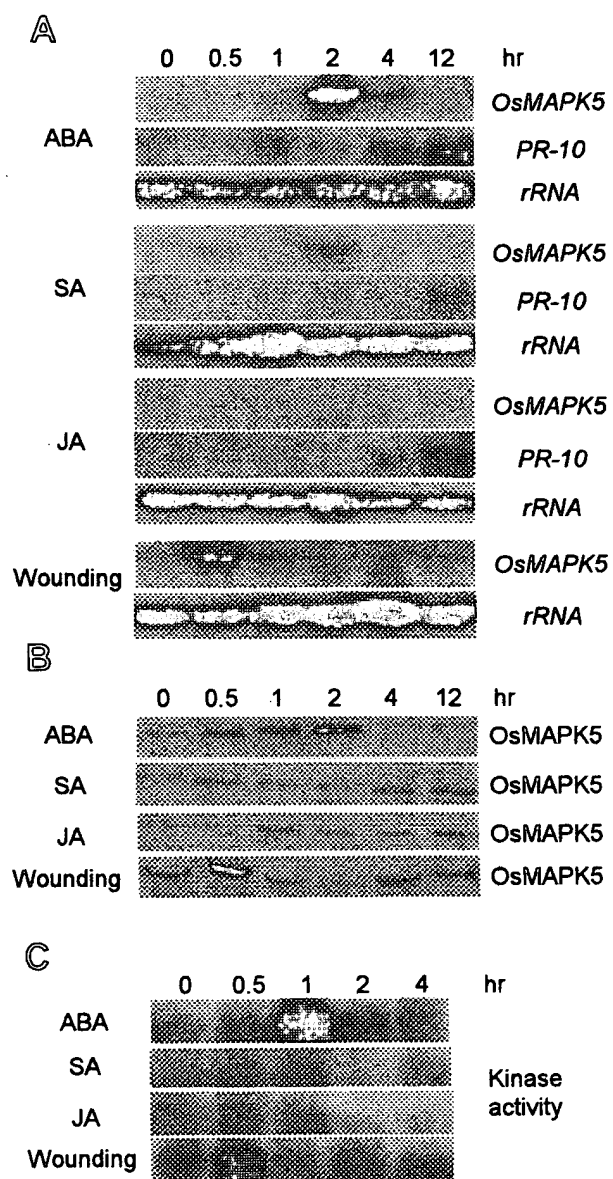
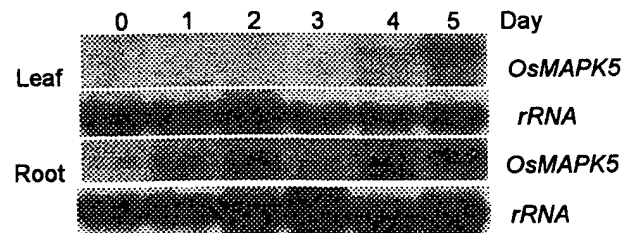
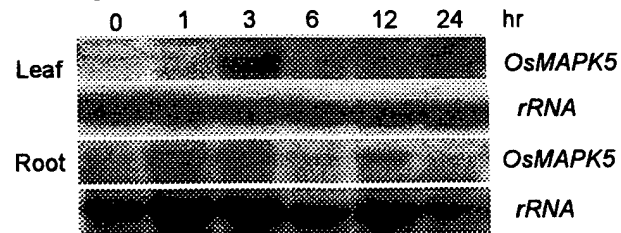
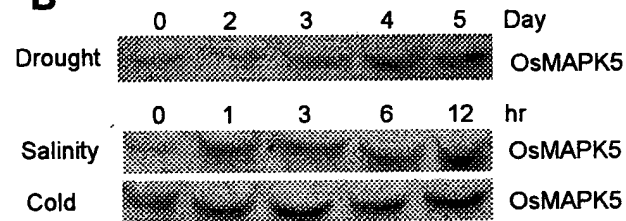
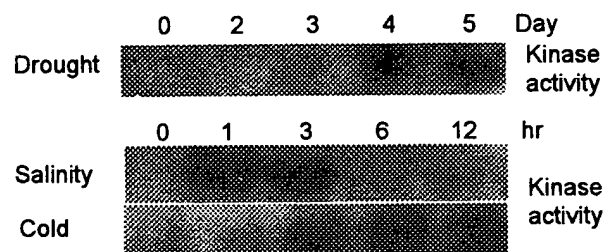


FIGURE 4

A**Drought****Salinity****Cold****B****C****FIGURE 5**

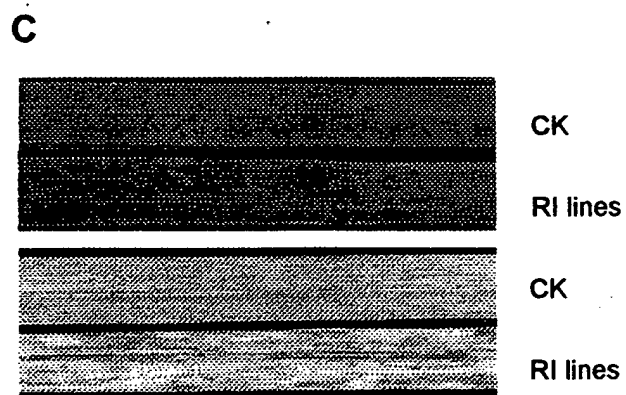
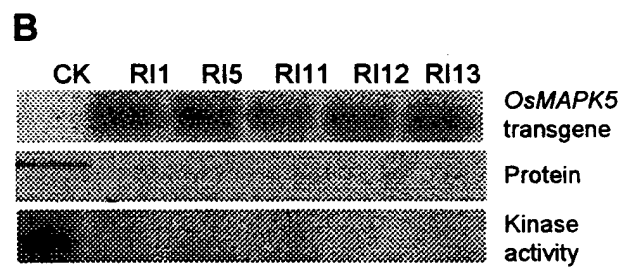
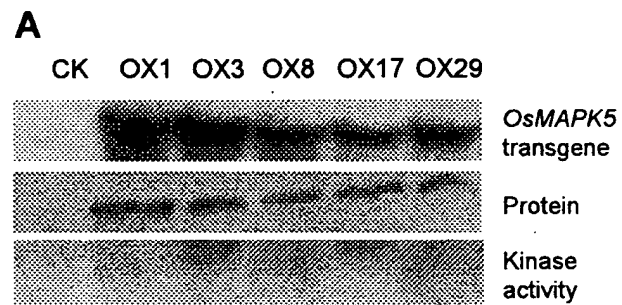
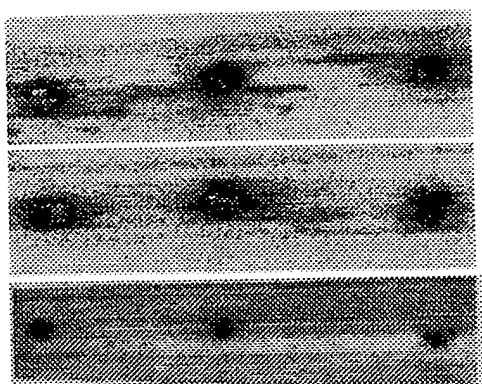
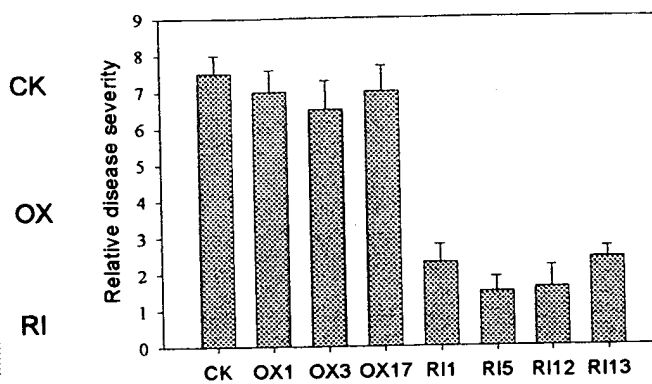
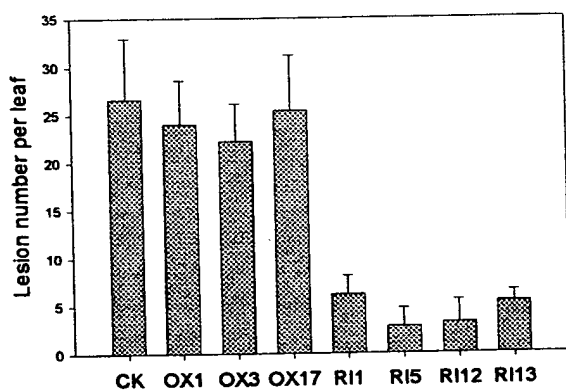
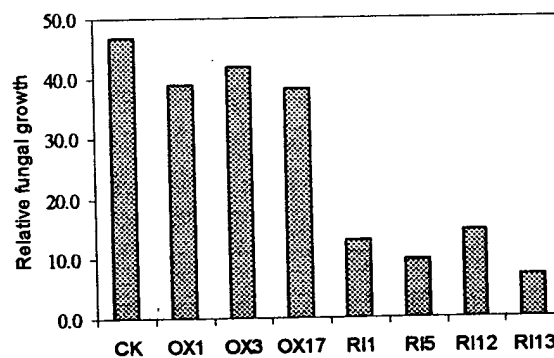
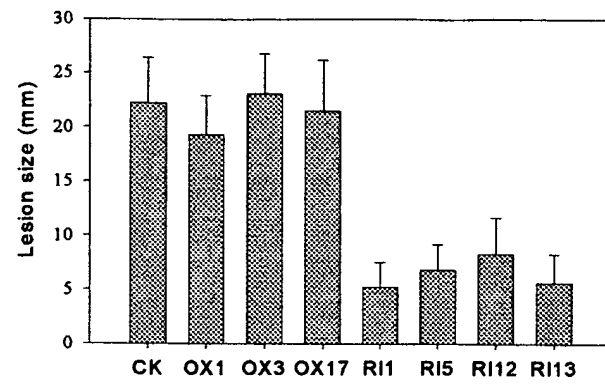
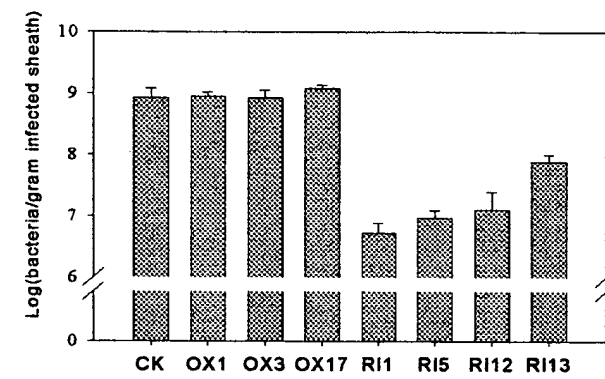


FIGURE 6

A**B****C****D****E****FIGURE 7**

A**B****C****FIGURE 8**

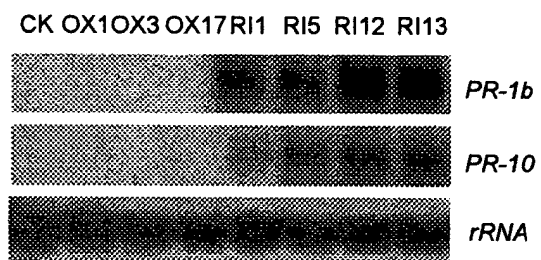
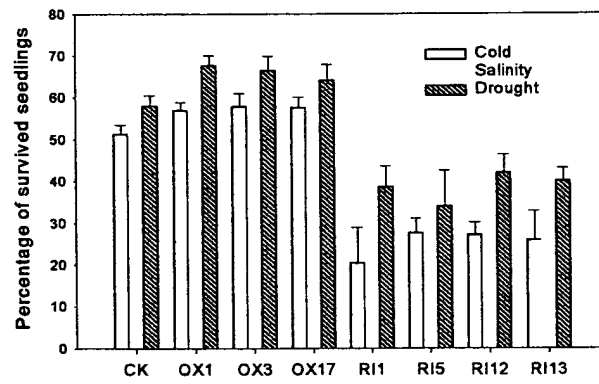
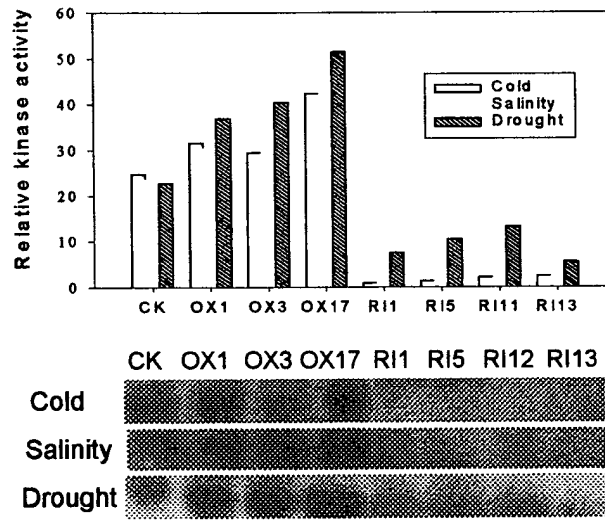


FIGURE 9

A**B****FIGURE 10**

OsMAPK5a
SEQ. ID. NO: 1

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1      agagagtcag ataaggctcgt taattagggtt ggtcaattcg gctgcttgcg gcgagagaag
61     aggaggaggg attagggatg gacggggcgc cggtggcgga gttcaggccg acgatgacgc
121    acggcggccg gtacctgctc tacgacatct tcggaacaa gttcgagggtg acgaacaagt
181    accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtgatga
241    actttgagac gagggagatg gtggcgataa agaagatcgc caacgcgttc aacaacgaca
301    tggacgcca ggcacgctc cgggagatca agctcctcag gcacctcgac caccgagaaca
361    tcataggcat cagggatgtg atcccgcgcg cgatccctca ggcgttcaac gacgtctaca
421    tcgccacgga gctcatggac accgacctcc atcacatcat ccgctccaac caagaactgt
481    cagaagagca ctgccagtat ttcctgtacc agatcctgcg ggggctcaag tacatccact
541    cggcgaacgt gatccaccgc gacctgaagc cgagcaacct gctgctgaac gccaaactgcg
601    acctcaagat ctgcgacttc gggctggcgc ggccgtcgtc ggagagcgac atgatgacgg
661    agtacgtggg caccgggtgg taccgcgcgc cggagctgct gctcaactcc accgactact
721    ccgccgccat cgacgtctgg tccgtcggct gcatcttcat ggagctcatc aaccgccagc
781    cgctcttccc cggcagggac cacatgcacc agatgcgcct catcaccgag gtgatcggga
841    cgccgacgga cgacgagctg gggttcatac ggaacgagga cgcgaggaag tacatgaggc
901    acctgccca gtaccgcgc cggacgttcg cgagcatgtt cccgcgggtg cagcccgcg
961    cgctcgacct catcgagagg atgctcacct tcaaccgcgt gcagagaatc acagttgagg
1021   aggcgctcga tcatccttac ctagagagat tgcacgacat cgccgatgag cccatctgcc
1081   tggagccctt ctccttcgac ttcgagcaga aggctctaaa cgaggaccaa atgaagcagc
1141   tgatcttcaa cgaagcgatc gagatgaacc caaacatccg gtactagatt gaatcaccat
1201   ggaaatgaga tcccgtctat acctgctttg tacatatgat caagattgag agccgggtag
1261   actgaacatt gcatttgttt gtttgttgat gttcgaaacc cacattctct gcaagttgtg
1321   gctgctttgt atgatatatg gtactatggt cgaataaaaag ggtttggaac tttggattaa
1381   aaaaaaaaaa aaaaaa

```

FIGURE 11

OsMAPK5a
SEQ. ID. NO: 2

MDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGR
GAYGIVCSVMNFETREMVAIKKIANAFNNDMDAKRTLREIKLLRHLDHENIIGIRDVI
PPPIPQAFNDVYIATELMDTDLHHIIRSNQELSEHCQYFLYQILRGLKYIHSANVIH
RDLKPSNLLLNNANCDLKICDFGLARPSSSESDMMTEYVVTRWYRAPELLNSTDYSAAI
DVWSVGCI FMELINRQPLFPGRDHMHQMLITEVIGTPTDDELGFIRNEDARKYMRHL
PQYPRRTFASMFP RVQPAALDLIERMLTFNPLQRITVEEALDHPYLERLHDIAD EPIC
LEPFSFD FEQKALNEDQMKQLIFNEA IEMNPNI RY

FIGURE 12

OsMAPK5b
SEQ. ID. NO: 3

```

1      agagagtcag ataaggtcgt taattagggtt ggtcaattcg gctgcttgcg gcgagagaag
61     aggaggaggg attagggatg gacggggcgc cggtggcgga gttcaggccg acgatgacgc
121    acggcgggccg gtacctgctc tacgacatct tcgggaacaa gttcgagggtg acgaacaagt
181    accagccgcc  catcatgccc attggccgcg  gcgcctacgg gatcgtctgc tccgtgatga
241    actttgagac gagggagatg gtggcgataa agaagatcgc caactgcgac ctcaagatct
301    gcgacttcgg gctggcgcg  ccgtcgtcgg agagcgacat gatgacggag tacgtggtca
361    cccggtggta ccgcgcgccg gagctgctgc tcaactccac cgactactcc gccgccatcg
421    acgtctggtc cgtcggctgc atcttcatgg agctcatcaa ccgccagccg ctcttccccg
481    gcagggacca catgcaccag atgcgcctca tcaccgaggt gatcgggacg ccgacggacg
541    acgagctggg gttcatacgg aacgaggacg cgaggaagta catgaggcac ctgccgcagt
601    acccgcgccg gacgttcgcg agcatgttcc cgcgggtgca gcccgccgcg ctcgacctca
661    tcgagaggat gctcaccttc aacccgctgc agagaatcac agttgaggag gcgctcgatc
721    atccttacct agagagattg cacgacatcg ccgatgagcc catctgcctg gagcccttct
781    ccttcgactt cgagcagaag gctctaaacg aggaccaa atgaagcagctg atcttcaacg
841    aagcgatcga gatgaaccca aacatccggt actagattga atcaccatgg aaatgagatc
901    ccgtctatac ctgctttgta catatgatca agattgagag ccgggtagac tgaacattgc
961    atttgtttgt ttgttgatgt tcgaaaccca cattctctgc aagttgtggc tgctttgtat
1021   gatatatggt actatgttcg aataaaaggg tttggaactt tggattaaaa aaaaaaaaaa
1081   aaaa

```

FIGURE 13

OsMAPK5b

SEQ. ID. NO: 4

MMDGAPVAEFRPTMTHGGRYLLYDIFGNKFEVTNKYQPPIMPIGR
GAYGIVCSVMNFETREMVAIKKIANCDLKICDFGLARPSSSESDMMTEYVVTRWYRAPE
LLNSTDYSAAIDVWSVGCI FMELINRQPLFPGRDHMHQMRLITEVIGTPTDDELGFI
RNEDARKYMRHLPQYPRRTFASMFPVQPAALDLIERMLTFNPLQRITVEEALDHPYL
ERLHDIADepICLEPFsFDfEQKALNEDQMKQLIFNEAIEMNPNIrY

FIGURE 14